

## LISTING OF CLAIMS

This listing of claims will replace all prior versions, and listings of claims in the application:

1-62. **(Canceled).**

63. **(Currently amended)** A method to identify a compound that modulates chromatin remodeling of a specific DNA sequence within chromatin comprising:

a) providing chromatin assembled DNA containing a specific DNA sequence, which specific DNA sequence comprises a binding site for a zinc finger DNA binding domain peptide of a nucleic acid regulatory protein, which zinc finger DNA binding domain peptide ~~immunoprecipitates~~interacts directly with a SWI/SNF chromatin remodeling complex comprising BRG1;

b) contacting the chromatin assembled DNA with:  
1) the SWI/SNF chromatin remodeling complex comprising BRG1, and  
2) the zinc finger DNA binding domain peptide of the nucleic acid regulatory protein;

under conditions that permit the direct interaction of the SWI/SNF chromatin remodeling complex and the zinc finger DNA binding domain peptide; and

c) determining the level of chromatin remodeling in the presence and absence of a test compound; wherein a difference in the level of chromatin remodeling in the presence and absence of the test compound identifies the test compound as a compound that modulates chromatin remodeling of the specific DNA sequence within chromatin.

64. **(Previously presented)** The method of claim 63, wherein the specific DNA sequence is an individual gene or portion thereof, a regulatory region or a chromosomal region.

65. **(Canceled).**

66. **(Previously presented)** The method of claim 63, wherein the nucleic acid regulatory protein is a transcription factor.

67-71. **(Canceled).**

72. **(Previously presented)** The method of claim 63, wherein the SWI/SNF chromatin remodeling complex is E-RC1.

73. **(Canceled).**

74. **(Currently amended)** The method of claim 63, wherein the SWI/SNF chromatin remodeling complex is a minimal SWI/SNF complex consisting of BRG1 and BAF155.

75-79. **(Canceled).**

80. **(Previously presented)** The method of claim 63, wherein the zinc finger DNA binding domain peptide is from GATA-1, Spl, EKLF, FKLf, BKLf, GKLF, LKLF, Wilm's tumor suppressor protein (WT1), BRCA1, BRCA2, KRAB, BTB/POZ, Zif268, GLI, Xfin, a BTB/POZ domain containing zinc finger protein, PLZF (promyelocytic leukemia zinc finger), or a nuclear hormone receptor.

81. **(Previously presented)** The method of claim 63, wherein the zinc finger DNA binding domain peptide is from a nuclear hormone receptor.

82. **(Previously presented)** The method of claim 81, wherein the nuclear hormone receptor is selected from the group consisting of an androgen, estrogen, thyroid, progesterone, and glucocorticoid receptor.

83. **(Previously presented)** The method of claim 63, wherein the zinc finger DNA binding domain peptide binds to a promoter, an enhancer, an insulator, a silencer, or locus of control regions (LCRs).

84. **(Previously presented)** The method of claim 63, wherein the test compound is a small molecule.

85. **(Previously presented)** The method of claim 63, wherein the test compound is a peptide.

86-87. **(Canceled).**

88. **(Previously presented)** The method of claim 63, wherein the amount of chromatin remodeling is determined by assaying for DNase hypersensitive sites within the specific DNA sequence.

89-102. **(Canceled).**

103. **(Previously presented)** The method of claim 63, wherein the zinc finger DNA binding domain peptide is from GATA-1, Spl, or EKLF.

104. **(Previously presented)** The method of claim 63, wherein the zinc finger DNA binding domain peptide is from GATA-1 or EKLF.

105. **(Previously presented)** The method of claim 63, wherein the zinc finger DNA binding domain peptide is from EKLF.

106. **(New)** The method of claim 63, wherein the SWI/SNF chromatin remodeling complex is a minimal SWI/SNF complex consisting of BRG1 and BAF155; and wherein the zinc finger DNA binding domain peptide is from GATA-1, Spl, or EKLF.